



2618-102-PUS.ST25.txt
SEQUENCE LISTING

<110> Sim, Gek-Kee
Dreitz, Matthew J.

<120> T CELL RECEPTOR PROTEINS, NUCLEIC ACID MOLECULES, AND USES
THEREOF

<130> 2618-102-PUS

<140> 09/744,847

<141> 2001-01-29

<150> PCT/US99/17309

<151> 1999-07-29

<150> 60/094,506

<151> 1998-07-29

<160> 111

<170> PatentIn version 3.3

<210> 1

<211> 381

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(381)

<400> 1

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Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu	
1 5 10 15	
ttg aac gca caa gtg act caa acc ccg aga caa ctc atc aaa aaa gtg	96
Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val	
20 25 30	
gga gcg aaa gtt ttg ttg aaa tgt tca cag aat atg gac cat gaa aga	144
Gly Ala Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg	
35 40 45	
atg ttc tgg tat cga caa gac cca ggt ctg ggg ttg cgg ctg ctc tac	192
Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr	
50 55 60	
tgg tcc tat aat att gac agt gtt gag aca gga gac atc cct tat ggg	240
Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly	
65 70 75 80	
tac agt gtc tcg agg aag aag aag gat gcc ttc ccc ttg att ctg gag	288
Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu	
85 90 95	
tct gct cgc atc aac cag aca tct gtg tac ttc tgc gcc agc agc ccg	336

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Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Pro
100 105 110

ttt agc caa aat acc cag tac ttc ggg gcg ggc acc cgg ctg cta 381
Phe Ser Gln Asn Thr Gln Tyr Phe Gly Ala Gly Thr Arg Leu Leu
115 120 125

<210> 2
<211> 127
<212> PRT
<213> Canis familiaris

<400> 2

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1 5 10 15

Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val
20 25 30

Gly Ala Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg
35 40 45

Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr
50 55 60

Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly
65 70 75 80

Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu
85 90 95

Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Pro
100 105 110

Phe Ser Gln Asn Thr Gln Tyr Phe Gly Ala Gly Thr Arg Leu Leu
115 120 125

<210> 3
<211> 381
<212> DNA
<213> Canis familiaris

<400> 3

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gaagtacaca gatgtctggt tgatgcgagc agactccaga atcaagggga aggcatacctt 120

cttcttcctc gagacactgt acccataagg gatgtctcct gtctcaacac tgtcaatatt 180

<212> PRT

<213> Canis familiaris

<400> 5

Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
 1 5 10 15

Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
 20 25 30

Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe
 35 40 45

Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
 50 55 60

Asn Gln Gly Ala Glu Ala Thr Tyr Glu Ser Gly Phe Thr Arg Glu Lys
 65 70 75 80

Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser
 85 90 95

Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Ser Ile Trp Tyr
 100 105 110

Gly Glu Gly Glu Gln His Phe Gly Pro Gly Thr Arg Leu Thr Val Leu
 115 120 125

<210> 6

<211> 408

<212> DNA

<213> Canis familiaris

<400> 6

taggacgggtg agccgggtcc ctggcccaaa gtgctgctcc ccctccccgt accaaatgct	60
gcagaagtaa gagctgggtgt cttcgaggct caggttgctc acagtcagag tggagaacat	120
taggggttcgg cggctgatgg gaaacttctc cctggtaaatt ccacttttcgt aggtggcctc	180
tgcaccctgg tttgcgggtg caatcagtat caagctctgt cctgggagct gacggtacca	240
gaacatcaag gtgacttggg tatcgacctc acagtggatg gtaatggagg tcccacgttg	300
acagatgtcc ctgcgcggct tttgagagac aagagctcca aacacagagc cttgtcccag	360
gaggagtagc aggcaagtca gcatctttag gtgctagccc ttcaccgt	408

<210> 7

<211> 384
 <212> DNA
 <213> Canis familiaris

<220>
 <221> exon
 <222> (1)..(384)

<400> 7
 atg ctg act tgc ctg cta ctc ctc ctg gga caa ggc tct gtg ttt gga 48
 Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
 1 5 10 15
 gct ctt gtc tct caa aag ccg cgc agg gac atc tgt caa cgt ggg acc 96
 Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
 20 25 30
 tcc att acc atc cac tgt gag gtc gat acc caa gtc acc ttg atg ttc 144
 Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe
 35 40 45
 tgg tac cgt cag ctc cca gga cag agc ttg ata ctg att gca acc gca 192
 Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
 50 55 60
 aac cag ggt gca gag gcc acc tac gaa agt gga ttt acc agg gag aag 240
 Asn Gln Gly Ala Glu Ala Thr Tyr Glu Ser Gly Phe Thr Arg Glu Lys
 65 70 75 80
 ttt ccc atc agc cgc cga acc cta atg ttc tcc act ctg act gtg agc 288
 Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser
 85 90 95
 aac ctg agc ctc gaa gac acc agc tct tac ttc tgc agc att tgg tac 336
 Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Ser Ile Trp Tyr
 100 105 110
 ggg gag ggg gag cag cac ttt ggg cca ggg acc cgg ctc acc gtc cta 384
 Gly Glu Gly Glu Gln His Phe Gly Pro Gly Thr Arg Leu Thr Val Leu
 115 120 125

<210> 8
 <211> 384
 <212> DNA
 <213> Canis familiaris

<400> 8
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 tagggttcgg cggctgatgg gaaacttctc cctggtaaata ccactttcgt aggtggcctc 180
 tgcaccctgg tttgcggttg caatcagtat caagctctgt cctgggagct gacggtacca 240
 gaacatcaag gtgacttggg tatcgacctc acagtggatg gtaatggagg tcccacgttg 300

acagatgtcc ctgcgcggct tttgagagac aagagctcca aacacagagc cttgtcccag 360
gaggagtagc aggcaagtca gcat 384

<210> 9
<211> 408
<212> DNA
<213> Canis familiaris

<220>
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<222> (7)..(408)

<400> 9
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Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu
1 5 10

tgg aca gga tac atg gat gct gga att atc cag agc cca aga tac aag 96
Trp Thr Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys
15 20 25 30

gtc aca ggg aca gga aag agg gtg act ctg aga tgt cac cag aca gac 144
Val Thr Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp
35 40 45

aac tat gac tat atg tac tgg tat cga cat gac ctg gga cat ggg ccg 192
Asn Tyr Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro
50 55 60

agg ctg atc tat tat tca aat ggt att aac agc act gaa aaa gga gac 240
Arg Leu Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp
65 70 75

ctc tcc aat gga tac aca gtc tct aga tca aac aag atg gat ttc ccc 288
Leu Ser Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro
80 85 90

ctc cta ctg gac tct gtt acc tcc tcc cag aca tct gtg tac ttc tgt 336
Leu Leu Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys
95 100 105 110

gcc gac acg agg gat cct gtt gca gta aat tat gat ttt aac ttt ggc 384
Ala Asp Thr Arg Asp Pro Val Ala Val Asn Tyr Asp Phe Asn Phe Gly
115 120 125

cca ggg acc aag ctg aca gtc gta 408
Pro Gly Thr Lys Leu Thr Val Val
130

<210> 10
<211> 134
<212> PRT
<213> Canis familiaris

<400> 10

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Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu Trp Thr
1 5 10 15

Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys Val Thr
20 25 30

Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp Asn Tyr
35 40 45

Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro Arg Leu
50 55 60

Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp Leu Ser
65 70 75 80

Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro Leu Leu
85 90 95

Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Ala Asp
100 105 110

Thr Arg Asp Pro Val Ala Val Asn Tyr Asp Phe Asn Phe Gly Pro Gly
115 120 125

Thr Lys Leu Thr Val Val
130

<210> 11
<211> 408
<212> DNA
<213> Canis familiaris

<400> 11
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ggggaaatcc atcttgtttg atctagagac tgtgtatcca ttggagaggt ctcctttttc 180
agtgtgttta ataccatttg aataatagat cagcctcggc ccatgtccca ggcatgtcg 240
ataccagtac atatagtcac agttgtctgt ctggtgacat ctcagagtca ccctctttcc 300
tgtccctgtg accttgatc ttgggctctg gataattcca gcatccatgt atcctgtcca 360
caggacacaa agagccatgc caaagaagac gccggtggcc atttcagc 408

<210> 12

<211> 402
 <212> DNA
 <213> Canis familiaris

<220>
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 <222> (1)..(402)

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 1 5 10 15
 gga tac atg gat gct gga att atc cag agc cca aga tac aag gtc aca 96
 Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys Val Thr
 20 25 30
 ggg aca gga aag agg gtg act ctg aga tgt cac cag aca gac aac tat 144
 Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp Asn Tyr
 35 40 45
 gac tat atg tac tgg tat cga cat gac ctg gga cat ggg ccg agg ctg 192
 Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro Arg Leu
 50 55 60
 atc tat tat tca aat ggt att aac agc act gaa aaa gga gac ctc tcc 240
 Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp Leu Ser
 65 70 75 80
 aat gga tac aca gtc tct aga tca aac aag atg gat ttc ccc ctc cta 288
 Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro Leu Leu
 85 90 95
 ctg gac tct gtt acc tcc tcc cag aca tct gtg tac ttc tgt gcc gac 336
 Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Ala Asp
 100 105 110
 acg agg gat cct gtt gca gta aat tat gat ttt aac ttt ggc cca ggg 384
 Thr Arg Asp Pro Val Ala Val Asn Tyr Asp Phe Asn Phe Gly Pro Gly
 115 120 125
 acc aag ctg aca gtc gta 402
 Thr Lys Leu Thr Val Val
 130

<210> 13
 <211> 402
 <212> DNA
 <213> Canis familiaris

<400> 13
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 cctcgtgtcg gcacagaagt acacagatgt ctgggaggag gtaacagagt ccagtaggag 120
 ggggaaatcc atcttggttg atctagagac tgtgtatcca ttggagaggt ctcctttttc 180

2016-2021 RefSeq chr10

agtgcgtgta ataccatttg aataatagat cagcctcggc ccatgtccca ggcatgtcg	240
ataccagtac atatagtcac agttgtctgt ctggtgacat ctccagagtc cctctttcc	300
tgtccctgtg accttgatc ttgggctctg gataattcca gcatccatgt atcctgtcca	360
caggacacaa agagccatgc caaagaagac gccggtggcc at	402

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<210> 14
<211> 483
<212> DNA
<213> Canis familiaris
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<220>
<221> CDS
<222> (85) .. (483)
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<210> 15
 <211> 133
 <212> PRT
 <213> Canis familiaris

<400> 15

Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala
 1 5 10 15

Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys
 20 25 30

Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His
 35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe
 50 55 60

Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro
 65 70 75 80

Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu
 85 90 95

Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
 100 105 110

Ser Leu Asp Ala Phe Asp Ala Gly Gln Leu Tyr Phe Gly Ala Gly Ser
 115 120 125

Lys Leu Ala Val Leu
 130

<210> 16
 <211> 483
 <212> DNA
 <213> Canis familiaris

<400> 16

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gctgctggca cagagatata gggctgagtc tcctggctcc agggagttca tctccagctg 120

ggagctgtag ttactgaact gctgcactga gaatcttgcc gggatgtctc ctttgtctct 180

ctcttcccta ttgtaatact gaatgagaaa ccggggaccc tggcccaggg cctgttggtgta 240

ccagtacaca gatagggtgtc cagagataag ggaacatctc agggtcactg tctgtcctct 300

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tgctttgatc atgtgtcttg gagtttggat gacctcagac tccacggggc cggctcccag 360
gagacaaagg gccacacagc agagaagcct ggagcccatg gcagccctgg gaagctgata 420
gcctccccgc tcctcgtgcc gcggtggagc tccagctttt gttcccttta gtgaggggta 480
att 483

<210> 17
<211> 399
<212> DNA
<213> Canis familiaris

<220>
<221> exon
<222> (1)..(399)

<400> 17
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Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala
1 5 10 15
ggc ccc gtg gag tct gag gtc atc caa act cca aga cac atg atc aaa 96
Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys
20 25 30
gca aga gga cag aca gtg acc ctg aga tgt tcc ctt atc tct gga cac 144
Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His
35 40 45
cta tct gtg tac tgg tac caa cag gcc ctg ggc cag ggt ccc cgg ttt 192
Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe
50 55 60
ctc att cag tat tac aat agg gaa gag aga gac aaa gga gac atc ccg 240
Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro
65 70 75 80
gca aga ttc tca gtg cag cag ttc agt aac tac agc tcc cag ctg gag 288
Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu
85 90 95
atg aac tcc ctg gag cca gga gac tca gcc cta tat ctc tgt gcc agc 336
Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110
agc tta gat gcg ttc gac gcg ggg cag ctg tac ttc ggg gcc ggt tcc 384
Ser Leu Asp Ala Phe Asp Ala Gly Gln Leu Tyr Phe Gly Ala Gly Ser
115 120 125
aag ctg gcc gtg ctg 399
Lys Leu Ala Val Leu
130

<210> 18
<211> 399

<212> DNA

<213> Canis familiaris

<400> 18

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gctgctggca cagagatata gggctgagtc tcttggctcc agggagttca tctccagctg      120
ggagctgtag ttactgaact gctgcactga gaatcttgcc gggatgtctc ctttgtctct      180
ctcttcctta ttgtaatact gaatgagaaa cgggggaccc tggcccaggg cctgttggtta      240
ccagtacaca gataggtgtc cagagataag ggaacatctc agggtcactg tctgtcctct      300
tgctttgatc atgtgtcttg gagtttggat gacctcagac tccacggggc cggctcccag      360
gagacaaagg gccacacagc agagaagcct ggagcccat                               399

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<210> 19

<211> 462

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (73)..(462)

<400> 19

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catcacctga ag atg ctg atg ctt ctg ctg ctc ctg ggg ccc agc tct gga      111
          Met Leu Met Leu Leu Leu Leu Leu Gly Pro Ser Ser Gly
          1              5              10

ctc ggt gcc ctc gtc ttc cag gcg ccc agc aca atg atc tgt aag agc      159
Leu Gly Ala Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser
    15              20              25

gga gcc acc gtg cag atc cag tgt caa aca gtg gac ctt caa gcc aca      207
Gly Ala Thr Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr
    30              35              40              45

acc gtg ttt tgg tat cgc cag ctc ccg aag cag ggc ctt acc ctt atg      255
Thr Val Phe Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met
          50              55              60

gtg acc tct aac gtg ggc aac agt gct aca cac gag cag ggg ttc cct      303
Val Thr Ser Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro
          65              70              75

gca gcc aag ttc cct gtt aac cac cca aac ctc acg ttt tcc tcc ctg      351
Ala Ala Lys Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu
          80              85              90

atg gtg acg agt tca ggt cct gga gac agc ggc ctc tac ttc tgt ggt      399
Met Val Thr Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys Gly
          95              100              105

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gtt cgg gcg tat ggt ggg aac tcg ccc ctc tac ttt gga aca ggc acc 447
Val Arg Ala Tyr Gly Gly Asn Ser Pro Leu Tyr Phe Gly Thr Gly Thr
110 115 120 125

agg ctc acc gtg aca 462
Arg Leu Thr Val Thr
130

<210> 20
<211> 130
<212> PRT
<213> Canis familiaris

<400> 20

Met Leu Met Leu Leu Leu Leu Leu Gly Pro Ser Ser Gly Leu Gly Ala
1 5 10 15

Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser Gly Ala Thr
20 25 30

Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr Thr Val Phe
35 40 45

Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met Val Thr Ser
50 55 60

Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro Ala Ala Lys
65 70 75 80

Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu Met Val Thr
85 90 95

Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys Gly Val Arg Ala
100 105 110

Tyr Gly Gly Asn Ser Pro Leu Tyr Phe Gly Thr Gly Thr Arg Leu Thr
115 120 125

Val Thr
130

<210> 21
<211> 462
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<213> Canis familiaris

<400> 21

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tgtcacggtg agcctggtgc ctgttccaaa gtagaggggc gagttcccac catacgcccg      60
aacaccacag aagtagaggc cgctgtctcc aggacctgaa ctcgtcacca tcagggagga      120
aaacgtgagg tttgggtggt taacaggga cttggctgca gggaaccct gctcgtgtgt      180
agcactgttg cccacgttag aggtcaccat aagggttaagg ccctgcttcg ggagctggcg      240
ataccaaaac acggttgttg cttgaaggct cactgtttga cactggatct gcacggtggc      300
tccgctctta cagatcattg tgctgggcgc ctggaagacg agggcaccga gtccagagct      360
gggccccagg agcagcagaa gcatcagcat cttcagggtga tggcctcata ccatacctct      420
ctcaagatag atatgaccac gcctcgtgcc gaatcctgca gc                          462

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<210> 22
<211> 417
<212> DNA
<213> Canis familiaris

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<220>
<221> CDS
<222> (13)..(417)

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<400> 22
cacgagcctg cc atg tgc cca gtg ttc atc tgc tcc ttg gtc ctc tgg ctc      51
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           1               5               10

ctg agt aca ggc acc ctc aat gca aaa gtc atg cag act cca gga cat      99
Leu Ser Thr Gly Thr Leu Asn Ala Lys Val Met Gln Thr Pro Gly His
  15               20               25

ctg gtc aaa ggg aaa gga caa aaa gca aaa atg gaa tgt gtc cca ata      147
Leu Val Lys Gly Lys Gly Gln Lys Ala Lys Met Glu Cys Val Pro Ile
  30               35               40               45

aaa gga cat agt tat gtt ttc tgg tat cag cag atc cca gca aaa gag      195
Lys Gly His Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu
          50               55               60

ttc aag ttc ttg att tct ttc cag gat aac gct gtc ttt gat aaa aca      243
Phe Lys Phe Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr
          65               70               75

ggg atg ccc acg cag aga ttt tta gcc ttg tgt cca aaa aac cta ccc      291
Gly Met Pro Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro
          80               85               90

tgt agc cta gag atc gag cgt aca gag ctg cag gat tca gcc gtg tat      339
Cys Ser Leu Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr
          95               100              105

ttt tgt gcc agc agt gac aga act ggg gga ctc gtt cac gag cag tat      387
Phe Cys Ala Ser Ser Asp Arg Thr Gly Gly Leu Val His Glu Gln Tyr
  110               115               120              125

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ttc ggc gcc ggc acc agg ctc acg gtc ctc
 Phe Gly Ala Gly Thr Arg Leu Thr Val Leu
 130 135

<210> 23
 <211> 135
 <212> PRT
 <213> Canis familiaris

<400> 23

Met Cys Pro Val Phe Ile Cys Ser Leu Val Leu Trp Leu Leu Ser Thr
 1 5 10 15

Gly Thr Leu Asn Ala Lys Val Met Gln Thr Pro Gly His Leu Val Lys
 20 25 30

Gly Lys Gly Gln Lys Ala Lys Met Glu Cys Val Pro Ile Lys Gly His
 35 40 45

Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu Phe Lys Phe
 50 55 60

Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr Gly Met Pro
 65 70 75 80

Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro Cys Ser Leu
 85 90 95

Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr Phe Cys Ala
 100 105 110

Ser Ser Asp Arg Thr Gly Gly Leu Val His Glu Gln Tyr Phe Gly Ala
 115 120 125

Gly Thr Arg Leu Thr Val Leu
 130 135

<210> 24
 <211> 417
 <212> DNA
 <213> Canis familiaris

<400> 24

gaggaccgtg agcctgggtgc cggcgccgaa atactgctcg tgaacgagtc ccccgattct 60

gtcactgctg gcacaaaaat acacggctga atcctgcagc tctgtacgct cgatctctag 120

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gctacagggg aggttttttg gacacaaggc taaaaatctc tgcgtgggca tccctgtttt 180
atcaaagaca gcgttatcct ggaaagaaat caagaacttg aactcttttg ctgggatctg 240
ctgataccag aaaacataac tatgtccttt tattgggaca cattccattt ttgctttttg 300
tcctttccct ttgaccagat gtcttgagat ctgcatgact tttgcattga ggggtgcctgt 360
actcaggagc cagaggacca aggagcagat gaacactggg cacatggcag gctcgtg 417

<210> 25
<211> 423
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (40)..(423)

<400> 25
ggcacgagca ctgaggacca gactgtgcct gtctccacc atg ggc tcc ggg ttc 54
Met Gly Ser Gly Phe
1 5

ctc tgc tgt atg gtc ctc tgc ctc ctg gga gca gca ccc ctg gac aca 102
Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala Ala Pro Leu Asp Thr
10 15 20

aca gtt tcc cag act cca aga tac ctc atc gcg cac gtg gga tcg aag 150
Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala His Val Gly Ser Lys
25 30 35

aag tta cta aaa tgt gag caa aat ctg ggc cat aat gct atg tac tgg 198
Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His Asn Ala Met Tyr Trp
40 45 50

tat aag caa gac ctc aag caa ctg ctg aag atc atg ttt atc tac ttt 246
Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile Met Phe Ile Tyr Phe
55 60 65

aat cag gga ctc aat cta aat gaa tca gtt cca ggt cgt ttc tca cct 294
Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro Gly Arg Phe Ser Pro
70 75 80 85

gag aca ctg aca agc tca tta act tca tgt cga ctc ctg aac agt gac 342
Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg Leu Leu Asn Ser Asp
90 95 100

tct gct gtg tat ttc tgt gcc agc agc gag ggg tat gat gaa aaa ttg 390
Ser Ala Val Tyr Phe Cys Ala Ser Ser Glu Gly Tyr Asp Glu Lys Leu
105 110 115

tat ttt gca agt gga acc aag ctt tct gtc ttg 423
Tyr Phe Ala Ser Gly Thr Lys Leu Ser Val Leu
120 125

<210> 26
 <211> 128
 <212> PRT
 <213> Canis familiaris

<400> 26

Met Gly Ser Gly Phe Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala
 1 5 10 15

Ala Pro Leu Asp Thr Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala
 20 25 30

His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His
 35 40 45

Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile
 50 55 60

Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro
 65 70 75 80

Gly Arg Phe Ser Pro Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg
 85 90 95

Leu Leu Asn Ser Asp Ser Ala Val Tyr Phe Cys Ala Ser Ser Glu Gly
 100 105 110

Tyr Asp Glu Lys Leu Tyr Phe Ala Ser Gly Thr Lys Leu Ser Val Leu
 115 120 125

<210> 27
 <211> 423
 <212> DNA
 <213> Canis familiaris

<400> 27

caagacagaa agcttggttc cacttgcaaa atacaatttt tcatcatacc cctcgctgct 60
 ggcacagaaa tacacagcag agtcactgtt caggagtcga catgaagtta atgagcttgt 120
 cagtgtctca ggtgagaaac gacctggaac tgattcattt agattgagtc cctgattaaa 180
 gtagataaac atgatcttca gcagttgctt gaggtcttgc ttataaccagt acatagcatt 240
 atggcccaga ttttgctcac attttagtaa cttcttcgat cccacgtgcg cgatgaggta 300
 tcttgaggtc tgggaaactg ttgtgtccag ggggtgctgct cccaggaggc agaggaccat 360
 acagcagagg aaccgggagc ccatggtgga gacaggcaca gtctggtcct cagtgtctcg 420

gcc

<210> 28
 <211> 333
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(333)

<400> 28
 atc gga ctc ctc tgt ggt gtg gcc ttt tgt ttc ctg gga gta ggc ctt 48
 Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu
 1 5 10 15
 ttg aac gca caa gtg act caa acc ccg aga caa ctc atc aaa aaa gtg 96
 Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val
 20 25 30
 gga gcg aaa gtt ttg ttg aaa tgt tca cag aat atg gac cat gaa aga 144
 Gly Ala Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg
 35 40 45
 atg ttc tgg tat cga caa gac cca ggt ctg ggg ttg cgg ctg ctc tac 192
 Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr
 50 55 60
 tgg tcc tat aat att gac agt gtt gag aca gga gac atc cct tat ggg 240
 Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly
 65 70 75 80
 tac agt gtc tcg agg aag aag aag gat gcc ttc ccc ttg att ctg gag 288
 Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu
 85 90 95
 tct gct cgc atc aac cag aca tct gtg tac ttc tgc gcc agc agc 333
 Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser
 100 105 110

<210> 29
 <211> 111
 <212> PRT
 <213> Canis familiaris

<400> 29

Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu
 1 5 10 15
 Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val
 20 25 30

Gly Ala Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg

35

40

45

Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr
 50 55 60

Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly
 65 70 75 80

Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu
 85 90 95

Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser
 100 105 110

<210> 30

<211> 333

<212> DNA

<213> Canis familiaris

<400> 30

gctactggcg cagaagtaca cagatgtctg gttgatgcca gcagactcca gaatcaaggg 60

gaaggcatcc ttcttcttcc tcgagacact gtaccataa gggatgtctc ctgtctcaac 120

actgtcaata ttataggacc agtagagcag ccgcaacccc agacctgggt cttgtcgata 180

ccagaacatt ctttcatggt ccatattctg tgaacatttc aacaaaactt tcgctcccac 240

ttttttgatg agttgtctcg gggtttgagt cacttgtgcy ttcaaaaggc ctactcccag 300

gaaacaaaag gccacaccac agaggagtcc gat 333

<210> 31

<211> 351

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (25)..(351)

<400> 31

acggtgaagg gctagcacct aaag atg ctg act tgc ctg cta ctc ctc ctg 51

Met Leu Thr Cys Leu Leu Leu Leu
 1 5

gga caa ggc tct gtg ttt gga gct ctt gtc tct caa aag ccg cgc agg 99

Gly Gln Gly Ser Val Phe Gly Ala Leu Val Ser Gln Lys Pro Arg Arg
 10 15 20 25

gac atc tgt caa cgt ggg acc tcc att acc atc cac tgt gag gtc gat 147

Asp Ile Cys Gln Arg Gly Thr Ser Ile Thr Ile His Cys Glu Val Asp

30

35

40

acc caa gtc acc ttg atg ttc tgg tac cgt cag ctc cca gga cag agc 195
 Thr Gln Val Thr Leu Met Phe Trp Tyr Arg Gln Leu Pro Gly Gln Ser
 45 50 55

ttg ata ctg att gca acc gca aac cag ggt gca gag gcc acc tac gaa 243
 Leu Ile Leu Ile Ala Thr Ala Asn Gln Gly Ala Glu Ala Thr Tyr Glu
 60 65 70

agt gga ttt acc agg gag aag ttt ccc atc agc cgc cga acc cta atg 291
 Ser Gly Phe Thr Arg Glu Lys Phe Pro Ile Ser Arg Arg Thr Leu Met
 75 80 85

ttc tcc act ctg act gtg agc aac ctg agc ctc gaa gac acc agc tct 339
 Phe Ser Thr Leu Thr Val Ser Asn Leu Ser Leu Glu Asp Thr Ser Ser
 90 95 100 105

tac ttc tgc agc 351
 Tyr Phe Cys Ser

<210> 32
 <211> 109
 <212> PRT
 <213> Canis familiaris

<400> 32

Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
 1 5 10 15

Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
 20 25 30

Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe
 35 40 45

Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
 50 55 60

Asn Gln Gly Ala Glu Ala Thr Tyr Glu Ser Gly Phe Thr Arg Glu Lys
 65 70 75 80

Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser
 85 90 95

Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Ser
 100 105

<210> 33

<211> 351
 <212> DNA
 <213> Canis familiaris

<400> 33
 gctgcagaag taagagctgg tgtcttcgag gctcagggtg ctcacagtca gagtggagaa 60
 cattaggggtt cggcggctga tgggaaactt ctccctggta aatccacttt cgtaggtggc 120
 ctctgcaccc tggtttgctg ttgcaatcag tatcaagctc tgtcctggga gctgacggta 180
 ccagaacatc aaggtgactt gggatcgcac ctcacagtgg atggtaatgg aggtcccacg 240
 ttgacagatg tccctgcgcg gcttttgaga gacaagagct ccaaacacag agccttgtcc 300
 caggaggagt agcaggcaag tcagcatctt taggtgctag cccttcaccg t 351

<210> 34
 <211> 339
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (7)..(339)

<400> 34
 gctgaa atg gcc acc ggc gtc ttc ttt ggc atg gct ctt tgt gtc ctg 48
 Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu
 1 5 10
 tgg aca gga tac atg gat gct gga att atc cag agc cca aga tac aag 96
 Trp Thr Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys
 15 20 25 30
 gtc aca ggg aca gga aag agg gtg act ctg aga tgt cac cag aca gac 144
 Val Thr Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp
 35 40 45
 aac tat gac tat atg tac tgg tat cga cat gac ctg gga cat ggg ccg 192
 Asn Tyr Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro
 50 55 60
 agg ctg atc tat tat tca aat ggt att aac agc act gaa aaa gga gac 240
 Arg Leu Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp
 65 70 75
 ctc tcc aat gga tac aca gtc tct aga tca aac aag atg gat ttc ccc 288
 Leu Ser Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro
 80 85 90
 ctc cta ctg gac tct gtt acc tcc tcc cag aca tct gtg tac ttc tgt 336
 Leu Leu Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys
 95 100 105 110
 gcc 339
 Ala

<210> 35
 <211> 111
 <212> PRT
 <213> Canis familiaris

<400> 35

Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu Trp Thr
 1 5 10 15

Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys Val Thr
 20 25 30

Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp Asn Tyr
 35 40 45

Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro Arg Leu
 50 55 60

Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp Leu Ser
 65 70 75 80

Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro Leu Leu
 85 90 95

Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Ala
 100 105 110

<210> 36
 <211> 339
 <212> DNA
 <213> Canis familiaris

<400> 36

ggcacagaag tacacagatg tctgggagga ggtaacagag tccagtagga gggggaaatc 60
 catcttgttt gatctagaga ctgtgtatcc attggagagg tctccttttt cagtgtgttt 120
 aataccattt gaataataga tcagcctcgg cccatgtccc aggtcatgtc gataccagta 180
 catatagtca tagttgtctg tctggtgaca tctcagagtc accctctttc ctgtccctgt 240
 gaccttgat cttgggctct ggataattcc agcatccatg taccctgtcc acaggacaca 300
 aagagccatg ccaaagaaga cgccggtggc catttcagc 339

<210> 37
 <211> 423

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (85)..(423)

<400> 37

aattaaccct cactaaaggg aacaaaagct ggagctccac cgcggcacga ggagcgggga 60

ggctatcagc ttcccagggc tgcc atg ggc tcc agg ctt ctc tgc tgt gtg 111

Met Gly Ser Arg Leu Leu Cys Cys Val
1 5

gcc ctt tgt ctc ctg gga gcc ggc ccc gtg gag tct gag gtc atc caa 159

Ala Leu Cys Leu Leu Gly Ala Gly Pro Val Glu Ser Glu Val Ile Gln
10 15 20 25

act cca aga cac atg atc aaa gca aga gga cag aca gtg acc ctg aga 207

Thr Pro Arg His Met Ile Lys Ala Arg Gly Gln Thr Val Thr Leu Arg
30 35 40

tgt tcc ctt atc tct gga cac cta tct gtg tac tgg tac caa cag gcc 255

Cys Ser Leu Ile Ser Gly His Leu Ser Val Tyr Trp Tyr Gln Gln Ala
45 50 55

ctg ggc cag ggt ccc cgg ttt ctc att cag tat tac aat agg gaa gag 303

Leu Gly Gln Gly Pro Arg Phe Leu Ile Gln Tyr Tyr Asn Arg Glu Glu
60 65 70

aga gac aaa gga gac atc ccg gca aga ttc tca gtg cag cag ttc agt 351

Arg Asp Lys Gly Asp Ile Pro Ala Arg Phe Ser Val Gln Gln Phe Ser
75 80 85

aac tac agc tcc cag ctg gag atg aac tcc ctg gag cca gga gac tca 399

Asn Tyr Ser Ser Gln Leu Glu Met Asn Ser Leu Glu Pro Gly Asp Ser
90 95 100 105

gcc cta tat ctc tgt gcc agc agc 423

Ala Leu Tyr Leu Cys Ala Ser Ser
110

<210> 38

<211> 113

<212> PRT

<213> Canis familiaris

<400> 38

Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala
1 5 10 15Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys
20 25 30

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Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His
35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe
50 55 60

Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro
65 70 75 80

Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu
85 90 95

Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

Ser

<210> 39
<211> 423
<212> DNA
<213> Canis familiaris

<400> 39
gctgctggca cagagatata gggctgagtc tcttggctcc agggagttca tctccagctg 60
ggagctgtag ttactgaact gctgcactga gaatcttgcc gggatgtctc ctttgtctct 120
ctcttcccta ttgtaatact gaatgagaaa ccggggaccc tggcccaggg cctgttggtg 180
ccagtacaca gataggtgtc cagagataag ggaacatctc agggtcactg tctgtcctct 240
tgctttgatc atgtgtcttg gagtttggat gacctcagac tccacggggc cggctcccag 300
gagacaaaagg gccacacagc agagaagcct ggagcccatg gcagccctgg gaagctgata 360
gcctccccgc tctcgtgcc gcggtggagc tccagctttt gttcccttta gtgagggtta 420
att 423

<210> 40
<211> 396
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (73)..(396)

<400> 40
gctgcaggat tcggcacgag gcgtgggtcat atctatcttg agagaggtat ggtatgaggc 60

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catcacctga ag atg ctg atg ctt ctg ctg ctc ctg ggg ccc agc tct gga 111
Met Leu Met Leu Leu Leu Leu Gly Pro Ser Ser Gly
1 5 10

ctc ggt gcc ctc gtc ttc cag gcg ccc agc aca atg atc tgt aag agc 159
Leu Gly Ala Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser
15 20 25

gga gcc acc gtg cag atc cag tgt caa aca gtg gac ctt caa gcc aca 207
Gly Ala Thr Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr
30 35 40 45

acc gtg ttt tgg tat cgc cag ctc ccg aag cag ggc ctt acc ctt atg 255
Thr Val Phe Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met
50 55 60

gtg acc tct aac gtg ggc aac agt gct aca cac gag cag ggg ttc cct 303
Val Thr Ser Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro
65 70 75

gca gcc aag ttc cct gtt aac cac cca aac ctc acg ttt tcc tcc ctg 351
Ala Ala Lys Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu
80 85 90

atg gtg acg agt tca ggt cct gga gac agc ggc ctc tac ttc tgt 396
Met Val Thr Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys
95 100 105

<210> 41

<211> 108

<212> PRT

<213> Canis familiaris

<400> 41

Met Leu Met Leu Leu Leu Leu Gly Pro Ser Ser Gly Leu Gly Ala
1 5 10 15

Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser Gly Ala Thr
20 25 30

Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr Thr Val Phe
35 40 45

Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met Val Thr Ser
50 55 60

Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro Ala Ala Lys
65 70 75 80

Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu Met Val Thr
85 90 95

Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys
 100 105

<210> 42
 <211> 396
 <212> DNA
 <213> Canis familiaris

<400> 42
 acagaagtag aggccgctgt ctccaggacc tgaactcgtc accatcaggg aggaaaacgt 60
 gaggtttggg tggttaacag ggaacttggc tgcagggaac ccctgctcgt gtgtagcact 120
 gttgcccacg ttagagggtca ccataagggt aaggccctgc ttcgggagct ggcgatacca 180
 aaacacgggt gtggcttgaa ggtccactgt ttgacactgg atctgcacgg tggctccgct 240
 cttacagatc attgtgctgg gcgcctggaa gacgagggca ccgagtccag agctggggccc 300
 caggagcagc agaagcatca gcatcttcag gtgatggcct cataccatac ctctctcaag 360
 atagatatga ccacgcctcg tgccgaatcc tgcagc 396

<210> 43
 <211> 354
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (13)..(354)

<400> 43
 cacgagcctg cc atg tgc cca gtg ttc atc tgc tcc ttg gtc ctc tgg ctc 51
 Met Cys Pro Val Phe Ile Cys Ser Leu Val Leu Trp Leu
 1 5 10
 ctg agt aca ggc acc ctc aat gca aaa gtc atg cag act cca gga cat 99
 Leu Ser Thr Gly Thr Leu Asn Ala Lys Val Met Gln Thr Pro Gly His
 15 20 25
 ctg gtc aaa ggg aaa gga caa aaa gca aaa atg gaa tgt gtc cca ata 147
 Leu Val Lys Gly Lys Gly Gln Lys Ala Lys Met Glu Cys Val Pro Ile
 30 35 40 45
 aaa gga cat agt tat gtt ttc tgg tat cag cag atc cca gca aaa gag 195
 Lys Gly His Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu
 50 55 60
 ttc aag ttc ttg att tct ttc cag gat aac gct gtc ttt gat aaa aca 243
 Phe Lys Phe Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr
 65 70 75
 ggg atg ccc acg cag aga ttt tta gcc ttg tgt cca aaa aac cta ccc 291

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Gly Met Pro Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro
80 85 90

tgt agc cta gag atc gag cgt aca gag ctg cag gat tca gcc gtg tat 339
Cys Ser Leu Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr
95 100 105

ttt tgt gcc agc agt 354
Phe Cys Ala Ser Ser
110

<210> 44
<211> 114
<212> PRT
<213> Canis familiaris

<400> 44

Met Cys Pro Val Phe Ile Cys Ser Leu Val Leu Trp Leu Leu Ser Thr
1 5 10 15

Gly Thr Leu Asn Ala Lys Val Met Gln Thr Pro Gly His Leu Val Lys
20 25 30

Gly Lys Gly Gln Lys Ala Lys Met Glu Cys Val Pro Ile Lys Gly His
35 40 45

Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu Phe Lys Phe
50 55 60

Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr Gly Met Pro
65 70 75 80

Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro Cys Ser Leu
85 90 95

Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr Phe Cys Ala
100 105 110

Ser Ser

<210> 45
<211> 354
<212> DNA
<213> Canis familiaris

<400> 45
actgctggca caaaaataca cggctgaatc ctgcagctct gtacgctcga tctctaggct 60

2618-102-PUS.ST25.txt

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acagggtagg ttttttggac acaaggctaa aaatctctgc gtgggcatcc ctgttttatc 120
aaagacagcg ttatcctgga aagaaatcaa gaacttgaac tcttttgctg ggatctgctg 180
ataccagaaa acataactat gtccttttat tgggacacat tccatttttg ctttttgtcc 240
tttccctttg accagatgtc ctggagtctg catgactttt gcattgaggg tgccctgtact 300
caggagccag aggaccaagg agcagatgaa cactgggcac atggcaggct cgtg 354

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<210> 46
<211> 369
<212> DNA
<213> Canis familiaris

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<220>
<221> CDS
<222> (40)..(369)

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<400> 46
ggcacgagca ctgaggacca gactgtgcct gtctccacc atg ggc tcc ggg ttc 54
Met Gly Ser Gly Phe
1 5

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ctc tgc tgt atg gtc ctc tgc ctc ctg gga gca gca ccc ctg gac aca 102
Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala Ala Pro Leu Asp Thr
10 15 20

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aca gtt tcc cag act cca aga tac ctc atc gcg cac gtg gga tcg aag 150
Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala His Val Gly Ser Lys
25 30 35

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```

aag tta cta aaa tgt gag caa aat ctg ggc cat aat gct atg tac tgg 198
Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His Asn Ala Met Tyr Trp
40 45 50

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```

tat aag caa gac ctc aag caa ctg ctg aag atc atg ttt atc tac ttt 246
Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile Met Phe Ile Tyr Phe
55 60 65

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```

aat cag gga ctc aat cta aat gaa tca gtt cca ggt cgt ttc tca cct 294
Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro Gly Arg Phe Ser Pro
70 75 80 85

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```

gag aca ctg aca agc tca tta act tca tgt cga ctc ctg aac agt gac 342
Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg Leu Leu Asn Ser Asp
90 95 100

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```

tct gct gtg tat ttc tgt gcc agc agc 369
Ser Ala Val Tyr Phe Cys Ala Ser Ser
105 110

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<210> 47
<211> 110
<212> PRT
<213> Canis familiaris

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<400> 47

Met Gly Ser Gly Phe Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala
 1 5 10 15

Ala Pro Leu Asp Thr Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala
 20 25 30

His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His
 35 40 45

Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile
 50 55 60

Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro
 65 70 75 80

Gly Arg Phe Ser Pro Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg
 85 90 95

Leu Leu Asn Ser Asp Ser Ala Val Tyr Phe Cys Ala Ser Ser
 100 105 110

<210> 48

<211> 369

<212> DNA

<213> Canis familiaris

<400> 48

gctgctggca cagaaatata cagcagagtc actgttcagg agtcgacatg aagttaatga 60
 gcttgtcagt gtctcagggt agaaacgacc tggaactgat tcatttagat tgagtccctg 120
 attaaagtag ataaacatga tcttcagcag ttgcttgagg tcttgcttat accagtacat 180
 agcattatgg cccagatatt gtcacattt tagtaacttc ttcgatccca cgtgcgcgat 240
 gaggtatctt ggagtctggg aaactgttgt gtccaggggt gctgctccca ggaggcagag 300
 gaccatacag cagaggaacc cggagcccat ggtggagaca ggcacagtct ggtcctcagt 360
 gctcgtgcc 369

<210> 49

<211> 504

<212> DNA

<213> Canis familiaris

<400> 49

gaggatctgc agaaggcac ccctcccacg gtcacagtgt ttgaaccatc ggaagcagag 60

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atctcgcgga cccagaaggc cacactcgtg tgccctggcca cgggcttcta ccccgaccac	120
gtggagctga gctgggtgggt gaacgggaag gaggtcacga gtgggttcag caccgacccg	180
cagccctaca aggagaggcc cagcgagaat gactccagct actgtctgag cagccggctg	240
agggtctctg cctccttctg gcacaacccg cgcaaccact tcgctgcca agtccagttc	300
tatgggctcg gggacgacga tgagtggaaa tacgatagag tcaaaccat caccagaac	360
atcagtgtg aggcctgggg cagagcagac tgtggcttca cctcgggtgc ctaccatcag	420
ggcgtcctgt ctgccaccat cctctatgag atcctgctgg gcaaggccac gctgtatgct	480
gtgctgggtca gcatcctgggt gctg	504

<210> 50
 <211> 19
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 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 50	
cgacaagacc caggtctgg	19

<210> 51
 <211> 19
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 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 51	
gtcagctccc aggacagag	19

<210> 52
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 <212> DNA
 <213> Artificial

<220>
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<400> 52	
catgacctgg gacatgggc	19

<210> 53
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 53
 gagatgttcc cttatctctg g

21

<210> 54
 <211> 19
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 54
 cctctaacgt gggcaacag

19

<210> 55
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 55
 tcagcagatc ccagcaaaaag

20

<210> 56
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 56
 agcaagacct caagcaactg

20

<210> 57
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 57
 gtgaccttct gcagatcctc

20

<210> 58
 <211> 19
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 58
 agctcagctc cacgtggtc 19

<210> 59
 <211> 19
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 59
 tgctgaaccc actcgtgac 19

<210> 60
 <211> 109
 <212> PRT
 <213> Canis familiaris

<220>
 <221> MISC_FEATURE
 <222> (109)..(109)
 <223> At location 109, Xaa = Ala or Ser

<400> 60

Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu
 1 5 10 15

Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val
 20 25 30

Gly Arg Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg
 35 40 45

Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly
 50 55 60

Met Phe Trp Tyr Gln Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr
 65 70 75 80

Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu
 85 90 95

Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Xaa
 100 105

<210> 61
 <211> 110
 <212> PRT
 <213> Canis familiaris

<220>
 <221> MISC FEATURE
 <222> (109)..(110)
 <223> At locations 109 and 110, Xaa = Ala or Ser

<400> 61

Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu
 1 5 10 15

Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val
 20 25 30

Gly Arg Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg
 35 40 45

Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly
 50 55 60

Met Phe Trp Tyr Gln Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr
 65 70 75 80

Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu
 85 90 95

Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Xaa Xaa
 100 105 110

<210> 62
 <211> 111
 <212> PRT
 <213> Canis familiaris

<220>
 <221> MISC FEATURE
 <222> (109)..(111)
 <223> At locations 109, 110 and 111, Xaa = Ala or Ser

<400> 62

Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu
 1 5 10 15

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Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val
20 25 30

Gly Arg Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg
35 40 45

Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly
50 55 60

Met Phe Trp Tyr Gln Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr
65 70 75 80

Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu
85 90 95

Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Xaa Xaa Xaa
100 105 110

<210> 63
<211> 109
<212> PRT
<213> Canis familiaris

<220>
<221> MISC_FEATURE
<222> (109)..(109)
<223> At location 109, Xaa = Ala or Ser

<400> 63

Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
1 5 10 15

Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
20 25 30

Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe
35 40 45

Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
50 55 60

Ala Glu Ala Thr Tyr Glu Asn Gln Gly Ser Gly Phe Thr Arg Glu Lys
65 70 75 80

Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser

Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Xaa
 100 105

<210> 64
 <211> 110
 <212> PRT
 <213> Canis familiaris

<220>
 <221> MISC FEATURE
 <222> (109)..(110)
 <223> At locations 109 and 110, Xaa = Ala or Ser

<400> 64

Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
 1 5 10 15

Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
 20 25 30

Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe
 35 40 45

Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
 50 55 60

Ala Glu Ala Thr Tyr Glu Asn Gln Gly Ser Gly Phe Thr Arg Glu Lys
 65 70 75 80

Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser
 85 90 95

Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Xaa Xaa
 100 105 110

<210> 65
 <211> 111
 <212> PRT
 <213> Canis familiaris

<220>
 <221> MISC FEATURE
 <222> (109)..(111)
 <223> At locations 109, 110 and 111, Xaa = Ala or Ser

<400> 65

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Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
1          5          10          15

Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
          20          25          30

Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe
          35          40          45

Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
          50          55          60

Ala Glu Ala Thr Tyr Glu Asn Gln Gly Ser Gly Phe Thr Arg Glu Lys
65          70          75          80

Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser
          85          90          95

Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Xaa Xaa Xaa
          100          105          110

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<210> 66

<211> 111

<212> PRT

<213> Canis familiaris

<220>

<221> MISC_FEATURE

<222> (111)..(111)

<223> At location 111, Xaa = Ala or Ser

<400> 66

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Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu Trp Thr
1          5          10          15

Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys Val Thr
          20          25          30

Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp Asn Tyr
          35          40          45

Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro Arg Leu
50          55          60

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Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp Leu Ser
65 70 75 80

Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro Leu Leu
85 90 95

Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Xaa
100 105 110

<210> 67
<211> 112
<212> PRT
<213> Canis familiaris

<220>
<221> MISC_FEATURE
<222> (111)..(112)
<223> At locations 111 and 112, Xaa = Ala or Ser

<400> 67

Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu Trp Thr
1 5 10 15

Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys Val Thr
20 25 30

Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp Asn Tyr
35 40 45

Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro Arg Leu
50 55 60

Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp Leu Ser
65 70 75 80

Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro Leu Leu
85 90 95

Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Xaa Xaa
100 105 110

<210> 68
<211> 113
<212> PRT
<213> Canis familiaris

<220>

<221> MISC FEATURE

<222> (111)..(113)

<223> At locations 111, 112 and 113, Xaa = Ala or Ser

<400> 68

Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu Trp Thr
 1 5 10 15

Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys Val Thr
 20 25 30

Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp Asn Tyr
 35 40 45

Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro Arg Leu
 50 55 60

Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp Leu Ser
 65 70 75 80

Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro Leu Leu
 85 90 95

Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Xaa Xaa
 100 105 110

Xaa

<210> 69

<211> 111

<212> PRT

<213> Canis familiaris

<220>

<221> MISC FEATURE

<222> (111)..(111)

<223> At location 111, Xaa = Ala or Ser

<400> 69

Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala
 1 5 10 15

Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys
 20 25 30

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Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His
35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe
50 55 60

Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro
65 70 75 80

Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu
85 90 95

Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Xaa
100 105 110

<210> 70
<211> 112
<212> PRT
<213> Canis familiaris

<220>
<221> MISC_FEATURE
<222> (111)..(112)
<223> At locations 111 and 112, Xaa = Ala or Ser

<400> 70

Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys
20 25 30

Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His
35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe
50 55 60

Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro
65 70 75 80

Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu
85 90 95

Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Xaa Xaa

100

105

110

<210> 71
 <211> 113
 <212> PRT
 <213> Canis familiaris

<220>
 <221> MISC FEATURE
 <222> (111)..(113)
 <223> At locations 111, 112 and 113, Xaa = Ala or Ser

<400> 71

Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala
 1 5 10 15

Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys
 20 25 30

Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His
 35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe
 50 55 60

Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro
 65 70 75 80

Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu
 85 90 95

Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Xaa Xaa
 100 105 110

Xaa

<210> 72
 <211> 109
 <212> PRT
 <213> Canis familiaris

<220>
 <221> MISC FEATURE
 <222> (109)..(109)
 <223> At location 109, Xaa = Ala or Ser

<400> 72

Met Leu Met Leu Leu Leu Leu Gly Pro Ser Ser Gly Leu Gly Ala
 1 5 10 15

Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser Gly Ala Thr
 20 25 30

Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr Thr Val Phe
 35 40 45

Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met Val Thr Ser
 50 55 60

Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro Ala Ala Lys
 65 70 75 80

Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu Met Val Thr
 85 90 95

Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys Xaa
 100 105

<210> 73

<211> 110

<212> PRT

<213> Canis familiaris

<220>

<221> MISC_FEATURE

<222> (109)..(110)

<223> At locations 109 and 110, Xaa = Ala or Ser

<400> 73

Met Leu Met Leu Leu Leu Leu Gly Pro Ser Ser Gly Leu Gly Ala
 1 5 10 15

Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser Gly Ala Thr
 20 25 30

Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr Thr Val Phe
 35 40 45

Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met Val Thr Ser
 50 55 60

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Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro Ala Ala Lys
65 70 75 80

Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu Met Val Thr
85 90 95

Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys Xaa Xaa
100 105 110

<210> 74
<211> 111
<212> PRT
<213> Canis familiaris

<220>
<221> MISC_FEATURE
<222> (109)..(111)
<223> At locations 109, 110 and 111, Xaa = Ala or Ser

<400> 74

Met Leu Met Leu Leu Leu Leu Gly Pro Ser Ser Gly Leu Gly Ala
1 5 10 15

Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser Gly Ala Thr
20 25 30

Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr Thr Val Phe
35 40 45

Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met Val Thr Ser
50 55 60

Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro Ala Ala Lys
65 70 75 80

Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu Met Val Thr
85 90 95

Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys Xaa Xaa Xaa
100 105 110

<210> 75
<211> 112
<212> PRT
<213> Canis familiaris

<220>

<221> MISC FEATURE

<222> (112)..(112)

<223> At location 112, Xaa = Ala or Ser

<400> 75

Met	Cys	Pro	Val	Phe	Ile	Cys	Ser	Leu	Val	Leu	Trp	Leu	Leu	Ser	Thr
1				5					10					15	

Gly	Thr	Leu	Asn	Ala	Lys	Val	Met	Gln	Thr	Pro	Gly	His	Leu	Val	Lys
			20					25					30		

Gly	Lys	Gly	Gln	Lys	Ala	Lys	Met	Glu	Cys	Val	Pro	Ile	Lys	Gly	His
		35					40					45			

Ser	Tyr	Val	Phe	Trp	Tyr	Gln	Gln	Ile	Pro	Ala	Lys	Glu	Phe	Lys	Phe
	50					55					60				

Leu	Ile	Ser	Phe	Gln	Asp	Asn	Ala	Val	Phe	Asp	Lys	Thr	Gly	Met	Pro
65					70					75					80

Thr	Gln	Arg	Phe	Leu	Ala	Leu	Cys	Pro	Lys	Asn	Leu	Pro	Cys	Ser	Leu
				85					90					95	

Glu	Ile	Glu	Arg	Thr	Glu	Leu	Gln	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Xaa
			100					105					110		

<210> 76

<211> 113

<212> PRT

<213> Canis familiaris

<220>

<221> MISC FEATURE

<222> (112)..(113)

<223> At locations 112 nad 113, Xaa = Ala or Ser

<400> 76

Met	Cys	Pro	Val	Phe	Ile	Cys	Ser	Leu	Val	Leu	Trp	Leu	Leu	Ser	Thr
1				5					10					15	

Gly	Thr	Leu	Asn	Ala	Lys	Val	Met	Gln	Thr	Pro	Gly	His	Leu	Val	Lys
			20					25					30		

Gly	Lys	Gly	Gln	Lys	Ala	Lys	Met	Glu	Cys	Val	Pro	Ile	Lys	Gly	His
		35					40					45			

Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu Phe Lys Phe
 50 55 60

Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr Gly Met Pro
 65 70 75 80

Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro Cys Ser Leu
 85 90 95

Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr Phe Cys Xaa
 100 105 110

Xaa

<210> 77
 <211> 114
 <212> PRT
 <213> Canis familiaris

<220>
 <221> MISC_FEATURE
 <222> (112)..(114)
 <223> At locations 112, 113 and 114, Xaa = Ala or Ser

<400> 77

Met Cys Pro Val Phe Ile Cys Ser Leu Val Leu Trp Leu Leu Ser Thr
 1 5 10 15

Gly Thr Leu Asn Ala Lys Val Met Gln Thr Pro Gly His Leu Val Lys
 20 25 30

Gly Lys Gly Gln Lys Ala Lys Met Glu Cys Val Pro Ile Lys Gly His
 35 40 45

Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu Phe Lys Phe
 50 55 60

Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr Gly Met Pro
 65 70 75 80

Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro Cys Ser Leu
 85 90 95

Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr Phe Cys Xaa

100

Xaa Xaa

<210> 78
<211> 108
<212> PRT
<213> Canis familiaris

<220>
<221> MISC FEATURE
<222> (108)..(108)
<223> At location 108, Xaa = Ala or Ser

<400> 78

Met Gly Ser Gly Phe Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala
1 5 10 15

Ala Pro Leu Asp Thr Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala
20 25 30

His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His
35 40 45

Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile
50 55 60

Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro
65 70 75 80

Gly Arg Phe Ser Pro Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg
85 90 95

Leu Leu Asn Ser Asp Ser Ala Val Tyr Phe Cys Xaa
100 105

<210> 79
<211> 109
<212> PRT
<213> Canis familiaris

<220>
<221> MISC FEATURE
<222> (108)..(109)
<223> At locations 108 and 109, Xaa = Ala or Ser

<400> 79

Met Gly Ser Gly Phe Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala
 1 5 10 15

Ala Pro Leu Asp Thr Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala
 20 25 30

His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His
 35 40 45

Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile
 50 55 60

Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro
 65 70 75 80

Gly Arg Phe Ser Pro Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg
 85 90 95

Leu Leu Asn Ser Asp Ser Ala Val Tyr Phe Cys Xaa Xaa
 100 105

<210> 80

<211> 110

<212> PRT

<213> Canis familiaris

<220>

<221> MISC_FEATURE

<222> (108)..(110)

<223> At locations 108, 109 and 110, Xaa = Ala or Ser

<400> 80

Met Gly Ser Gly Phe Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala
 1 5 10 15

Ala Pro Leu Asp Thr Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala
 20 25 30

His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His
 35 40 45

Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile
 50 55 60

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Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro
65 70 75 80

Gly Arg Phe Ser Pro Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg
85 90 95

Leu Leu Asn Ser Asp Ser Ala Val Tyr Phe Cys Xaa Xaa Xaa
100 105 110

<210> 81
<211> 19
<212> DNA
<213> Artificial

<220>
<223> Synthetic Primer

<220>
<221> misc_feature
<222> (17)..(17)
<223> n = a

<400> 81
ccgaattctg gtaycrnca 19

<210> 82
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Synthetic Primer

<400> 82
cggatccgcr cartarta 18

<210> 83
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Synthetic Primer

<400> 83
cggatccgcr caraarta 18

<210> 84
<211> 19
<212> DNA
<213> Artificial

<220>
 <223> Synthetic Primer

<400> 84
 ccagacctgg gtcttgctg 19

<210> 85
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 85
 ctctgtcctg ggagctga 18

<210> 86
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 86
 ttgtttgatc tagagactgt g 21

<210> 87
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 87
 atcggactcc tctgtggtgt 20

<210> 88
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 88
 acggtgaagg gctagcacct 20

<210> 89
 <211> 20
 <212> DNA
 <213> Artificial

<220>
<223> Synthetic Primer

<400> 89
gctgaaatgg ccaccggcgt 20

<210> 90
<211> 19
<212> DNA
<213> Artificial

<220>
<223> Synthetic Primer

<400> 90
ctggtgccca cgtagagg 19

<210> 91
<211> 19
<212> DNA
<213> Artificial

<220>
<223> Synthetic Primer

<400> 91
ttactgaact gctgcactg 19

<210> 92
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Synthetic Primer

<400> 92
gctgcaggat tcggcacgag 20

<210> 93
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Synthetic Primer

<400> 93
tacgactgtc agcttggtcc 20

<210> 94
<211> 20
<212> DNA

<213> Artificial

<220>

<223> Synthetic Primer

<400> 94

cttttgctgg gatctgctga

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Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His Leu Ser Val Tyr Trp	
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Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe Leu Ile Gln Tyr Tyr	
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Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro Ala Arg Phe Ser Val	
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Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu Met Asn Ser Leu Glu	
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